

FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 17:50:39 ON 08 DEC 2004

L1 3168 S MCEWAN?/AU OR MCKERNAN?/AU
L2 23863 S "TWO HYBRID" OR "2 HYBRID" OR "INTERACTION TRAP SYSTEM"
L3 11377 S "GENOME WIDE" OR "PROTEOME WIDE" OR "PROTEIN INTERACTION MAP"
L4 55014 S "CDNA LIBRARY" OR "DNA GENOMIC LIBRARY" OR "GENOMIC LIBRARY"
L5 3841 S HYPERMETHYLATED OR HYPOMETHYLATED OR (METHIONINE (S) ENRICHED
L6 4 S BACTERIOMATCH
L7 10266 S "PROTEIN MAPPING" OR "PROTEIN MAP"
L8 16945 S "96" (S) WELL
L9 945 S "384" (S) WELL
L10 15407 S ("10,000" OR "1,000,000" OR 1,000?) (S) CELL?
L11 7 S L1 AND L2
L12 3 DUP REM L11 (4 DUPLICATES REMOVED)
L13 1 S L10 AND L5
L14 3 S L10 AND L2
L15 3 DUP REM L14 (0 DUPLICATES REMOVED)
L16 14 S L10 AND L3
L17 9 DUP REM L16 (5 DUPLICATES REMOVED)
L18 957 S "PROTEIN ARRAY"
L19 4 S L18 AND L10
L20 3 DUP REM L19 (1 DUPLICATE REMOVED)
L21 120 S L7 AND L2
L22 4 DUP REM L6 (0 DUPLICATES REMOVED)
L23 10 S L21 AND L4
L24 5 DUP REM L23 (5 DUPLICATES REMOVED)
L25 0 S L21 AND L5
L26 50 S L5 AND L3
L27 19 DUP REM L26 (31 DUPLICATES REMOVED)
L28 1 S L27 AND "REVIEW"
L29 252 S BAIT (P) PREY
L30 282 S BAIT AND PREY
L31 476 S 30 AND L2
L32 4 S L31 AND L3
L33 51 S L31 AND L4
L34 0 S L33 AND L18
L35 30 DUP REM L33 (21 DUPLICATES REMOVED)
L36 2 DUP REM L32 (2 DUPLICATES REMOVED)
L37 957 S "PROTEIN ARRAY"
L38 83394 S "PROTEIN INTERACTION"
L39 50 S L37 AND L38
L40 5 S L39 AND L2
L41 5 DUP REM L40 (0 DUPLICATES REMOVED)
L42 305 S (L8 OR L9) AND (MICROARRAY OR ARRAY)
L43 2 S L42 AND L38
L44 2 DUP REM L43 (0 DUPLICATES REMOVED)
L45 6263 S L38 AND L2
L46 537 S L45 AND "REPORTER"
L47 46 S L46 AND (L3 OR L4)
L48 36 DUP REM L47 (10 DUPLICATES REMOVED)
L49 28 S L48 NOT PY>=2003
L50 346 S "PROTEIN-PROTEIN" (S) MAP
L51 66 S L50 AND L2
L52 39 DUP REM L51 (27 DUPLICATES REMOVED)

=>

ANSWER 1 OF 5 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
 ACCESSION NUMBER: 2002:431982 BIOSIS
 DOCUMENT NUMBER: PREV200200431982
 TITLE: A novel pancreas Regeneration-(Reg-) binding protein.
 AUTHOR(S): Zhang, Hong [Reprint author]; Wu, Haiyan; Fan, Zuoheng;
 Patel, Sameer; Mueller, Cathy M. [Reprint author];
 Zenilman, Michael E. [Reprint author]
 CORPORATE SOURCE: Surgery, SUNY-Downstate Medical Center, 450 Clarkson Ave.,
 Brooklyn, NY, 11203, USA
 SOURCE: FASEB Journal, (March 22, 2002) Vol. 16, No. 5, pp. A1154.
 print.
 Meeting Info.: Annual Meeting of Professional Research
 Scientists on Experimental Biology. New Orleans, Louisiana,
 USA. April 20-24, 2002.
 CODEN: FAJOEC. ISSN: 0892-6638.
 DOCUMENT TYPE: Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LANGUAGE: English
 ENTRY DATE: Entered STN: 14 Aug 2002
 Last Updated on STN: 14 Aug 2002

AB Pancreas Regeneration (Reg) protein is secretory protein from acinar
 cells. It can stimulate ductal and islet beta-cell growth. In diabetic
 animal models, Reg I improves glucose tolerance. To study the mechanism
 of Reg I intracellular signaling, we employed the yeast-2-
hybrid system in ARIP, a rat ductal cell line which responds to
 Reg. The rat Reg coding sequence was cloned into the pBD-GAL4 Cam (bait)
 vector, and a **cDNA library** of the target cell ARIP was
 cloned in to the vector pAD-GAL4-2.1 (target). The clones were
 transformed into YRG-2 yeast, and assayed expression of LacZ reporter gene
 by the detection of beta-galactosidase activity. LacZ+ clone were
 isolated and sequenced. A homology search revealed that the entire DNA
 sequence of mitogen activating kinase phosphatase-1 (MKP-1) gene. We also
 demonstrated the association of Reg I with MKP-1 by co-
 immunoprecipitation. MKP-1 belongs to a class of dual-specificity
 phosphatase able to reverse the activation of mitogen-activated
protein (MAP) kinase family member and its function has
 been related to insulin gene regulation. We propose that pancreas Reg I
 protein exerts its mitogenic effect in ductal and beta cells through the
 MKP pathway.

L24 ANSWER 2 OF 5 MEDLINE on STN DUPLICATE 1
 ACCESSION NUMBER: 2002280109 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 12020817
 TITLE: HIV-1 integrase interacts with yeast microtubule-associated
 proteins.
 AUTHOR: de Soultrait Vaea Richard; Caumont Anne; Durrens Pascal;
 Calmels Christina; Parissi Vincent; Recordon Patricia; Bon
 Elisabeth; Desjobert Cecile; Tarrago-Litvak Laura; Fournier
 Michel
 CORPORATE SOURCE: UMR 5097 CNRS-Universite Victor Segalen Bordeaux 2, BP 103,
 Bat. 3A-3 Etage, 146 rue Leo Saignat, 33076 Bordeaux X
 Cedex, France.
 SOURCE: Biochimica et biophysica acta, (2002-May 3) 1575 (1-3) 40-8.
 Journal code: 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200207
 ENTRY DATE: Entered STN: 20020522
 Last Updated on STN: 20020720

Entered Medline: 20020719

AB The human immunodeficiency virus type 1 (HIV-1) integrase (IN) mediates the insertion of viral DNA into the human genome. In addition to IN, cellular and viral proteins are associated to proviral DNA in the so-called preintegration complex (PIC). We previously reported that the expression of HIV-1 IN in yeast leads to the emergence of a lethal phenotype. This effect may be linked to the IN activity on infected human cells where integration requires the cleavage of genomic DNA. To isolate and characterize potential cellular partners of HIV-1 IN, we used it as a bait in a **two-hybrid** system with a yeast **genomic library**. IN interacted with proteins belonging to the microtubule network, or involved in the protein synthesis apparatus. We focused our interest on one of the selected inserts, L2, which corresponds to the C-end half of the yeast STU2p, a microtubule-associated **protein (MAP)**. STU2p is an essential component of the yeast spindle pole body (SPB), which is able to bind microtubules in vitro. After expressing and purifying L2 as a recombinant protein, we showed its binding to IN by ELISA immunodetection. L2 was also able to inhibit IN activity in vitro. In addition, the effect of L2 was tested using the "lethal yeast phenotype". The coexpression of IN and the L2 peptide abolished the lethal phenotype, thus showing important in vivo interactions between IN and L2. The identification of components of the microtubule network associated with IN suggest a role of this complex in the transport of HIV-1 IN present in the PIC to the nucleus, as already described for other human viruses.

L24 ANSWER 3 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
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ACCESSION NUMBER: 2002177965 EMBASE
TITLE: HIV-1 integrase interacts with yeast microtubule-associated proteins.
AUTHOR: De Soultrait V.R.; Caumont A.; Durrens P.; Calmels C.; Parissi V.; Recordon P.; Bon E.; Desjobert C.; Tarrago-Litvak L.; Fournier M.
CORPORATE SOURCE: M. Fournier, UMR 5097 CNRS-Univ. V. S. Bordeaux 2, Bat. 3A-3 Etage, 146 rue Leo Saignat, 33076 Bordeaux Cedex, France. Michel.Fournier@reger.u-bordeaux2.fr
SOURCE: Biochimica et Biophysica Acta - Gene Structure and Expression, (3 May 2002) 1575/1-3 (40-48).
Refs: 43
ISSN: 0167-4781 CODEN: BBGSD5
PUBLISHER IDENT.: S 0167-4781(02)00241-5
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The human immunodeficiency virus type 1 (HIV-1) integrase (IN) mediates the insertion of viral DNA into the human genome. In addition to IN, cellular and viral proteins are associated to proviral DNA in the so-called preintegration complex (PIC). We previously reported that the expression of HIV-1 IN in yeast leads to the emergence of a lethal phenotype. This effect may be linked to the IN activity on infected human cells where integration requires the cleavage of genomic DNA. To isolate and characterize potential cellular partners of HIV-1 IN, we used it as a bait in a **two-hybrid** system with a yeast **genomic library**. IN interacted with proteins belonging to the microtubule network, or involved in the protein synthesis apparatus. We focused our interest on one of the selected inserts, L2, which corresponds to the C-end half of the yeast STU2p, a microtubule-associated **protein (MAP)**. STU2p is an essential component of the yeast spindle pole body (SPB), which is able to

bind microtubules in vitro. After expressing and purifying L2 as a recombinant protein, we showed its binding to IN by ELISA immunodetection. L2 was also able to inhibit IN activity in vitro. In addition, the effect of L2 was tested using the "lethal yeast phenotype". The coexpression of IN and the L2 peptide abolished the lethal phenotype, thus showing important in vivo interactions between IN and L2. The identification of components of the microtubule network associated with IN suggest a role of this complex in the transport of HIV-1 IN present in the PIC to the nucleus, as already described for other human viruses. .COPYRGHT. 2002 Elsevier Science B.V. All rights reserved.

L24 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 2
 ACCESSION NUMBER: 2001315015 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 11278711
 TITLE: A novel tobacco mitogen-activated **protein** (**MAP**) kinase kinase, NtMEK1, activates the cell cycle-regulated p43Ntf6 MAP kinase.
 AUTHOR: Calderini O; Glab N; Bergounioux C; Heberle-Bors E; Wilson C
 CORPORATE SOURCE: Institute of Microbiology and Genetics, University of Vienna, Dr. Bohrgasse 9, A-1030 Vienna, Austria.
 SOURCE: Journal of biological chemistry, (2001 May 25) 276 (21) 18139-45.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ302651
 ENTRY MONTH: 200107
 ENTRY DATE: Entered STN: 20010709
 Last Updated on STN: 20030105
 Entered Medline: 20010705

AB **Two-hybrid** screening of a tobacco BY-2 cell suspension **cDNA library** using the p43(Ntf6) mitogen-activated **protein (MAP)** kinase as bait resulted in the isolation of a cDNA encoding a protein with features characteristic of a MAP kinase kinase (MEK), which has been called NtMEK1. **Two-hybrid** interaction analysis and pull-down experiments showed a physical interaction between NtMEK1 and the tobacco MAP kinases p43(Ntf6) and p45(Ntf4), but not p43(Ntf3). In kinase assays NtMEK1 preferentially phosphorylated p43(Ntf6). Functional studies in yeast showed that p43(Ntf6) could complement the yeast MAP kinase mutant mpk1 when co-expressed with NtMEK1, and that this complementation depended on the kinase activity of p43(Ntf6). Expression analysis showed that the NtMEK1 and ntf6 genes are co-expressed both in plant tissues and following the induction of cell division in leaf pieces. These data suggest that NtMEK1 is an MEK for the p43(Ntf6) MAP kinase.

L24 ANSWER 5 OF 5 MEDLINE on STN DUPLICATE 3
 ACCESSION NUMBER: 1998250765 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 9582351
 TITLE: Regulation of protein phosphatase 2A activity by caspase-3 during apoptosis.
 AUTHOR: Santoro M F; Annand R R; Robertson M M; Peng Y W; Brady M J; Mankovich J A; Hackett M C; Ghayur T; Walter G; Wong W W; Giegel D A
 CORPORATE SOURCE: Department of Biochemistry, Parke-Davis Pharmaceutical Research Division, Warner-Lambert Company, Ann Arbor, Michigan 48105, USA.
 SOURCE: Journal of biological chemistry, (1998 May 22) 273 (21) 13119-28.

Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 20000303
Entered Medline: 19980625

AB Although the available evidence suggests that whereas the caspase family plays a major role in apoptosis, they are not the sole stimulators of death. A random yeast **two-hybrid** screen of a lymphocyte **cDNA library** (using caspase-3 as the bait) found an interaction between caspase-3 and the regulatory subunit Aalpha of protein phosphatase 2A. This protein was found to be a substrate for caspase-3, but not caspase-1, and could compete effectively against either a protein or synthetic peptide substrate. In Jurkat cells induced to undergo apoptosis with anti-Fas antibody, protein phosphatase 2A (PP2A) activity increased 4.5-fold after 6 h. By 12 h, the regulatory Aalpha subunit could no longer be detected in cell lysates. There was no change in the amount of the catalytic subunit. The effects on PP2A could be prevented by the caspase family inhibitors acetyl-Asp-Glu-Val-Asp (DEVD) aldehyde or Ac-DEVD fluoromethyl ketone. The mitogen-activated **protein (MAP)** kinase pathway is regulated by PP2A. At 12 h after the addition of anti-Fas antibody, a decrease in the amount of the phosphorylated forms of MAP kinase was observed. Again, this loss of activated MAP kinase could be prevented by the addition of DEVD-cho or DEVD-fmk. These data are consistent with a pathway whereby induction of apoptosis activates caspase-3. This enzyme then cleaves the regulatory Aalpha subunit of PP2A, increasing its activity. These data show that the activated PP2A will then effect a change in the phosphorylation state of the cell. These data provide a link between the caspases and signal transduction pathways.

ANSWER 2 OF 2 MEDLINE on STN DUPLICATE 1
 ACCESSION NUMBER: 2001545194 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 11559592
 TITLE: A protein-**protein interaction**
map of the *Caenorhabditis elegans* 26S proteasome.
 AUTHOR: Davy A; Bello P; Thierry-Mieg N; Vaglio P; Hitti J;
 Doucette-Stamm L; Thierry-Mieg D; Reboul J; Boulton S;
 Walhout A J; Coux O; Vidal M
 CORPORATE SOURCE: CRBM, CNRS UPR-1086, IFR 24, 34293 Montpellier, France.
 CONTRACT NUMBER: 232 (NHGRI)
 5R01HG01715-02 (NCI)
 7R33 CA81658-02 (NCI)
 P01CA80111-02
 SOURCE: EMBO reports, (2001 Sep) 2 (9) 821-8.
 Journal code: 100963049. ISSN: 1469-221X.
 PUB. COUNTRY: England: United Kingdom
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200112
 ENTRY DATE: Entered STN: 20011011
 Last Updated on STN: 20020122
 Entered Medline: 20011207

AB The ubiquitin-proteasome proteolytic pathway is pivotal in most biological processes. Despite a great level of information available for the eukaryotic 26S proteasome-the protease responsible for the degradation of ubiquitylated proteins-several structural and functional questions remain unanswered. To gain more insight into the assembly and function of the metazoan 26S proteasome, a **two-hybrid-based protein interaction map** was generated using 30 *Caenorhabditis elegans* proteasome subunits. The results recapitulate interactions reported for other organisms and reveal new potential interactions both within the 19S regulatory complex and between the 19S and 20S subcomplexes. Moreover, novel potential proteasome interactors were identified, including an E3 ubiquitin ligase, transcription factors, chaperone proteins and other proteins not yet functionally annotated. By providing a wealth of novel biological hypotheses, this interaction map constitutes a framework for further analysis of the ubiquitin-proteasome pathway in a multicellular organism amenable to both classical genetics and functional genomics.

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ANSWER 1 OF 5 MEDLINE on STN
 ACCESSION NUMBER: 2004399358 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 15290761
 TITLE: Discovering protein-protein interactions.
 AUTHOR: Ng See-Kiong; Tan Soon-Heng
 CORPORATE SOURCE: Knowledge Discovery Department, Institute for Infocomm Research, 21 Heng Mui Keng Terrace, Singapore 119613, Singapore.. skng@i2r.a-star.edu.sg
 SOURCE: J Bioinform Comput Biol, (2004 Jan) 1 (4) 711-41.
 Journal code: 101187344. ISSN: 0219-7200.
 PUB. COUNTRY: England: United Kingdom
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200409
 ENTRY DATE: Entered STN: 20040812
 Last Updated on STN: 20040921
 Entered Medline: 20040917

AB The ongoing genomics and proteomics efforts have helped identify many new genes and proteins in living organisms. However, simply knowing the existence of genes and proteins does not tell us much about the biological processes in which they participate. Many major biological processes are controlled by **protein interaction** networks. A comprehensive description of protein-protein interactions is therefore necessary to understand the genetic program of life. In this tutorial, we provide an overview of the various current high-throughput methods for discovering protein-protein interactions, covering both the conventional experimental methods and new computational approaches.

L41 ANSWER 2 OF 5 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
 ACCESSION NUMBER: 2004:348210 BIOSIS
 DOCUMENT NUMBER: PREV200400349961
 TITLE: Peptide aptamers: Specific inhibitors of protein function.
 AUTHOR(S): Hoppe-Seyler, Felix [Reprint Author]; Crnkovic-Mertens, Irena; Tomai, Evangelia; Butz, Karin
 CORPORATE SOURCE: Programm Infekt und Krebs, Deutsch Krebsforschungszentrum, Neuenheimer Feld 242, D-69120, Heidelberg, Germany
 hoppe-seyler@dkfz.de
 SOURCE: Current Molecular Medicine (Hilversum), (August 2004) Vol. 4, No. 5, pp. 529-538. print.
 ISSN: 1566-5240 (ISSN print).
 DOCUMENT TYPE: Article
 General Review; (Literature Review)
 LANGUAGE: English
 ENTRY DATE: Entered STN: 18 Aug 2004
 Last Updated on STN: 18 Aug 2004

L41 ANSWER 3 OF 5 MEDLINE on STN
 ACCESSION NUMBER: 2003465567 MEDLINE
 DOCUMENT NUMBER: PubMed ID: 14527327
 TITLE: Proteomics.
 AUTHOR: Zhu Heng; Bilgin Metin; Snyder Michael
 CORPORATE SOURCE: Department of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, Connecticut 06520, USA.. heng.zhu@yale.edu
 SOURCE: Annual review of biochemistry, (2003) 72 783-812. Ref: 100
 Journal code: 2985150R. ISSN: 0066-4154.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, ACADEMIC)
 LANGUAGE: English

FILE SEGMENT: Priority Journals
ENTRY MONTH: 200312
ENTRY DATE: Entered STN: 20031008
Last Updated on STN: 20031218
Entered Medline: 20031209

AB Fueled by ever-growing DNA sequence information, proteomics-the large scale analysis of proteins-has become one of the most important disciplines for characterizing gene function, for building functional linkages between protein molecules, and for providing insight into the mechanisms of biological processes in a high-throughput mode. It is now possible to examine the expression of more than 1000 proteins using mass spectrometry technology coupled with various separation methods. High-throughput yeast **two-hybrid** approaches and analysis of protein complexes using affinity tag purification have yielded valuable protein-protein interaction maps. Large-scale protein tagging and subcellular localization projects have provided considerable information about protein function. Finally, recent developments in protein microarray technology provide a versatile tool to study protein-protein, protein-nucleic acid, protein-lipid, enzyme-substrate, and protein-drug interactions. Other types of microarrays, though not fully developed, also show great potential in diagnostics, protein profiling, and drug identification and validation. This review discusses high-throughput technologies for proteome analysis and their applications. Also discussed are the approaches used for the integrated analysis of the voluminous sets of data generated by proteome analysis conducted on a global scale.

L41 ANSWER 4 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
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ACCESSION NUMBER: 2000070588 EMBASE
TITLE: A comprehensive analysis of protein-protein interactions in *Saccharomyces cerevisiae*.
AUTHOR: Uetz P.; Giot L.; Cagney G.; Mansfield T.A.; Judson R.S.; Knight J.R.; Lockshon D.; Narayan V.; Srinivasan M.; Pochart P.; Qureshi-Emili A.; Li Y.; Godwin B.; Conover D.; Kalbfleisch T.; Vijayadamodar G.; Yang M.; Johnston M.; Fields S.; Rothberg J.M.
CORPORATE SOURCE: J.M. Rothberg, CuraGen Corporation, 555 Long Wharf Drive, New Haven, CT 06511, United States. jrothberg@curagen.com
SOURCE: Nature, (10 Feb 2000) 403/6770 (623-627).
Refs: 41
ISSN: 0028-0836 CODEN: NATUAS
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Two large-scale yeast **two-hybrid** screens were undertaken to identify protein-protein interactions between full-length open reading frames predicted from the *Saccharomyces cerevisiae* genome sequence. In one approach, we constructed a **protein array** of about 6,000 yeast transformants, with each transformant expressing one of the open reading frames as a fusion to an activation-domain. This array was screened by a simple and automated procedure for 192 yeast proteins, with positive responses identified by their positions in the array. In a second approach, we pooled cells expressing one of about 6,000 activation domain fusions to generate a library. We used a high-throughput screening procedure to screen nearly all of the 6,000 predicted yeast proteins, expressed as Gal4 DNA-binding domain fusion proteins, against the library, and characterized positives by sequence analysis. These approaches resulted in the detection of 957 putative interactions involving 1,004 *S. cerevisiae* proteins. These data reveal

interactions that place functionally unclassified proteins in a biological context, interactions between proteins involved in the same biological function, and interactions that link biological functions together into larger cellular processes. The results of these screens are shown here.

L41 ANSWER 5 OF 5 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
ACCESSION NUMBER: 2000:430423 BIOSIS
DOCUMENT NUMBER: PREV200000430423
TITLE: Genome-wide **protein interaction** maps.
using **two-hybrid** systems.
AUTHOR(S): Legrain, Pierre [Reprint author]; Selig, Luc
CORPORATE SOURCE: Hybrigenics, 180 Avenue Daumesnil, Paris, 75012, France
SOURCE: FEBS Letters, (25 August, 2000) Vol. 480, No. 1, pp. 32-36.
print.
CODEN: FEBLAL. ISSN: 0014-5793.
DOCUMENT TYPE: Article
General Review; (Literature Review)
LANGUAGE: English
ENTRY DATE: Entered STN: 11 Oct 2000
Last Updated on STN: 10 Jan 2002

AB Automated sequence technology has rendered functional biology amenable to genomic scale analysis. Among genome-wide exploratory approaches, the **two-hybrid** system in yeast (Y2H) has outranked other techniques because it is the system of choice to detect protein-protein interactions. Deciphering the cascade of binding events in a whole cell helps define signal transduction and metabolic pathways or enzymatic complexes. The function of proteins is eventually attributed through whole cell **protein interaction** maps where totally unknown proteins are partnered with fully annotated proteins belonging to the same functional category. Since its first description in the late 1980's, several versions of the Y2H have been developed in order to overcome the major limitations of the system, namely false positives and false negatives. Optimized versions have been recently applied at multi-molecular and genomic scale. These genome-wide surveys can be methodologically divided into two types of approaches: one either tests combinations of predefined polypeptides (the so-called matrix approach) using various short-cuts to speed up the process, or one screens with a given polypeptide (bait) for potential partners (preys) present in complex libraries of genomic or complementary DNA (library screening). In the former strategy, one tests what one knows, for example pair-wise interactions between full-length open reading frames from recently sequenced and annotated genomes. Although based on a one-by-one scheme, this method is reported to be amenable to large-scale genomics thanks to multicloning strategies and to the use of small robotics workstations. In the latter, highly complex cDNA or genomic libraries of protein domains can be screened to saturation with high-throughput screening systems allowing the discovery of yet unidentified proteins. Both approaches have strengths and drawbacks that will be discussed here. None yields a full proteome-wide screening since certain proteins (e.g. some transcription factors) are not usable in Y2H. Novel **two-hybrid** assays have been recently described in bacteria. Applications of these time- and cost-effective assays to genomic screening will be discussed and compared to the Y2H technology.

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Time: 11:53:21

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Additionally, enter the **first few letters** of the Inventor's First name.

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